



US-107
SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> GENES INVOLVED IN POLYSACCHARIDE PRODUCTION AND
UTILIZATION THEREOF

<130> US-107

<150> JP 2003-32075

<151> 2003-02-10

<160> 13

<170> PatentIn Ver. 2.0

<210> 1

<211> 1404

<212> DNA

<213> Methylophilus methylotrophus

<220>

<221> CDS

<222> (1)..(1404)

<400> 1

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ggg	agt	aat	cca	ctt	tac	atg	ctt	gag	tct	ctc	gtt	gag	ccc	ttg	gtg	96
Gly	Ser	Asn	Pro	Leu	Tyr	Met	Leu	Glu	Ser	Leu	Val	Glu	Pro	Leu	Val	
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atg	gtg	ttt	gtg	ctg	tgg	ggg	ttg	ttt	att	tat	acc	gaa	aac	cgc	att	144
Met	Val	Phe	Val	Leu	Trp	Gly	Leu	Phe	Ile	Tyr	Thr	Glu	Asn	Arg	Ile	
		35					40					45				
ccg	atg	tcg	att	ttt	att	aca	tcg	ata	gtg	ctg	ttt	tcg	att	tct	ttc	192
Pro	Met	Ser	Ile	Phe	Ile	Thr	Ser	Ile	Val	Leu	Phe	Ser	Ile	Ser	Phe	
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ccc	agc	ggc	gcc	aag	att	cgc	aag	ggc	ttt	gcc	aag	atg	tgc	cgg	gat	240
Pro	Ser	Gly	Ala	Lys	Ile	Arg	Lys	Gly	Phe	Ala	Lys	Met	Cys	Arg	Asp	
		65			70				75						80	
gtg	att	ggt	caa	tgg	ctg	gtc	att	gcc	acc	ttt	ttg	ctg	acc	ttt	gct	288
Val	Ile	Gly	Gln	Trp	Leu	Val	Ile	Ala	Thr	Phe	Leu	Leu	Thr	Phe	Ala	
			85						90					95		
tat	atc	act	cgt	tac	atc	acc	tta	tat	agc	gaa	aaa	tta	att	ctc	gcc	336
Tyr	Ile	Thr	Arg	Tyr	Ile	Thr	Leu	Tyr	Ser	Glu	Lys	Leu	Ile	Leu	Ala	
			100					105					110			
tgg	ttg	att	gtg	acg	cca	gtt	gcc	cag	att	att	gcg	ttg	cag	tta	cta	384
Trp	Leu	Ile	Val	Thr	Pro	Val	Ala	Gln	Ile	Ile	Ala	Leu	Gln	Leu	Leu	
		115					120					125				
aaa	tgg	gcc	agc	ccc	aaa	ttg	att	gag	tgg	caa	gga	cca	cga	caa	aac	432
Lys	Trp	Ala	Ser	Pro	Lys	Leu	Ile	Glu	Trp	Gln	Gly	Pro	Arg	Gln	Asn	
		130				135					140					
acc	ttg	att	atc	ggc	ttg	aat	gag	caa	ggt	ctg	ctt	ttg	gcg	gat	aat	480
Thr	Leu	Ile	Ile	Gly	Leu	Asn	Glu	Gln	Gly	Leu	Leu	Leu	Ala	Asp	Asn	

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145						150						155						160							
ctg	aaa	cgt	gat	tat	tat	caa	aga	atc	aat	ata	ttg	gga	ttt	ttt	gag	528									
Leu	Lys	Arg	Asp	Tyr	Tyr	Gln	Arg	Ile	Asn	Ile	Leu	Gly	Phe	Phe	Glu										
					165						170						175								
gac	cgc	gcg	cct	aac	cgg	ctt	ccg	cac	ata	gat	tct	tat	ccg	gta	ctt	576									
Asp	Arg	Ala	Pro	Asn	Arg	Leu	Pro	His	Ile	Asp	Ser	Tyr	Pro	Val	Leu										
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ggc	agc	ttg	aat	gaa	ctg	agt	cat	tac	ctg	aaa	tca	cac	act	gta	cac	624									
Gly	Ser	Leu	Asn	Glu	Leu	Ser	His	Tyr	Leu	Lys	Ser	His	Thr	Val	His										
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aaa	ctt	tat	atc	gct	tta	ccg	atg	tcc	agt	cac	cct	cgt	att	ttg	aaa	672									
Lys	Leu	Tyr	Ile	Ala	Leu	Pro	Met	Ser	Ser	His	Pro	Arg	Ile	Leu	Lys										
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Leu	Leu	Asp	Asp	Leu	Lys	Asp	Thr	Thr	Ala	Ser	Ile	Tyr	Phe	Val	Pro										
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gac	atc	ttt	gtc	acc	gac	ctg	atc	cag	gga	cgc	gtt	tcg	gat	gtc	aac	768									
Asp	Ile	Phe	Val	Thr	Asp	Leu	Ile	Gln	Gly	Arg	Val	Ser	Asp	Val	Asn										
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Gly	Ile	Pro	Val	Val	Ser	Val	Cys	Asp	Thr	Pro	Phe	Thr	Gly	Met	Asp										
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ggc	ttt	atc	aaa	cgc	acg	gca	gat	att	tta	ttt	tca	tta	ttg	gtg	ttg	864									
Gly	Phe	Ile	Lys	Arg	Thr	Ala	Asp	Ile	Leu	Phe	Ser	Leu	Leu	Val	Leu										
					275						280						285								
att	ctg	atc	tcg	cct	att	ttg	atc	ggc	att	gcg	att	gca	gta	aaa	ctc	912									
Ile	Leu	Ile	Ser	Pro	Ile	Leu	Ile	Gly	Ile	Ala	Ile	Ala	Val	Lys	Leu										
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acc	tct	cct	ggc	ccc	gtt	att	ttc	aag	caa	cgt	cgt	tac	ggc	ttg	gat	960									
Thr	Ser	Pro	Gly	Pro	Val	Ile	Phe	Lys	Gln	Arg	Arg	Tyr	Gly	Leu	Asp										
305						310						315						320							
gga	caa	cag	att	ttg	gtg	tac	aag	ttc	cgc	tcc	atg	acc	gtc	act	gaa	1008									
Gly	Gln	Gln	Ile	Leu	Val	Tyr	Lys	Phe	Arg	Ser	Met	Thr	Val	Thr	Glu										
					325						330						335								
gat	ggc	gca	acg	gtg	aca	caa	gcc	acc	agg	aat	gat	caa	cgc	att	acg	1056									
Asp	Gly	Ala	Thr	Val	Thr	Gln	Ala	Thr	Arg	Asn	Asp	Gln	Arg	Ile	Thr										
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cca	ctg	ggc	gcc	ttt	ttg	cgc	aaa	acc	tcc	ctg	gat	gag	ttg	ccg	cag	1104									
Pro	Leu	Gly	Ala	Phe	Leu	Arg	Lys	Thr	Ser	Leu	Asp	Glu	Leu	Pro	Gln										
					355						360						365								
ttt	att	aat	gtg	tta	caa	ggc	cgc	atg	agt	gtg	gtt	ggg	cca	cgc	cca	1152									
Phe	Ile	Asn	Val	Leu	Gln	Gly	Arg	Met	Ser	Val	Val	Gly	Pro	Arg	Pro										
					370						375						380								
cat	gcg	gtg	gcg	cat	aac	gag	gaa	tac	cgt	aag	ctg	att	aaa	ggc	tat	1200									
His	Ala	Val	Ala	His	Asn	Glu	Glu	Tyr	Arg	Lys	Leu	Ile	Lys	Gly	Tyr										
					385						390						395	400							
atg	gta	cgc	cac	aag	gta	aaa	ccc	ggg	att	acc	ggc	tggt	gca	cag	gta	1248									
Met	Val	Arg	His	Lys	Val	Lys	Pro	Gly	Ile	Thr	Gly	Trp	Ala	Gln	Val										
					405						410						415								
aat	ggc	ttc	cgc	ggc	gaa	acg	gac	acg	tta	gaa	aaa	atg	gag	caa	cgt	1296									
Asn	Gly	Phe	Arg	Gly	Glu	Thr	Asp	Thr	Leu	Glu	Lys	Met	Glu	Gln	Arg										
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gtc	cat	tat	gac	ctt	gag	tac	ctg	cgc	aac	tgg	agc	cct	cgc	ttg	gat	1344									
Val	His	Tyr	Asp	Leu	Glu	Tyr	Leu	Arg	Asn	Trp	Ser	Pro	Arg	Leu	Asp										
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 Gly Ala Tyr
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<210> 2

<211> 467

<212> PRT

<213> Methylophilus methylotrophus

<400> 2

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 20 25 30
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 35 40 45
 Pro Met Ser Ile Phe Ile Thr Ser Ile Val Leu Phe Ser Ile Ser Phe
 50 55 60
 Pro Ser Gly Ala Lys Ile Arg Lys Gly Phe Ala Lys Met Cys Arg Asp
 65 70 75 80
 Val Ile Gly Gln Trp Leu Val Ile Ala Thr Phe Leu Leu Thr Phe Ala
 85 90 95
 Tyr Ile Thr Arg Tyr Ile Thr Leu Tyr Ser Glu Lys Leu Ile Leu Ala
 100 105 110
 Trp Leu Ile Val Thr Pro Val Ala Gln Ile Ile Ala Leu Gln Leu Leu
 115 120 125
 Lys Trp Ala Ser Pro Lys Leu Ile Glu Trp Gln Gly Pro Arg Gln Asn
 130 135 140
 Thr Leu Ile Ile Gly Leu Asn Glu Gln Gly Leu Leu Leu Ala Asp Asn
 145 150 155 160
 Leu Lys Arg Asp Tyr Tyr Gln Arg Ile Asn Ile Leu Gly Phe Phe Glu
 165 170 175
 Asp Arg Ala Pro Asn Arg Leu Pro His Ile Asp Ser Tyr Pro Val Leu
 180 185 190
 Gly Ser Leu Asn Glu Leu Ser His Tyr Leu Lys Ser His Thr Val His
 195 200 205
 Lys Leu Tyr Ile Ala Leu Pro Met Ser Ser His Pro Arg Ile Leu Lys
 210 215 220
 Leu Leu Asp Asp Leu Lys Asp Thr Thr Ala Ser Ile Tyr Phe Val Pro
 225 230 235 240
 Asp Ile Phe Val Thr Asp Leu Ile Gln Gly Arg Val Ser Asp Val Asn
 245 250 255
 Gly Ile Pro Val Val Ser Val Cys Asp Thr Pro Phe Thr Gly Met Asp
 260 265 270
 Gly Phe Ile Lys Arg Thr Ala Asp Ile Leu Phe Ser Leu Leu Val Leu
 275 280 285
 Ile Leu Ile Ser Pro Ile Leu Ile Gly Ile Ala Ile Ala Val Lys Leu
 290 295 300
 Thr Ser Pro Gly Pro Val Ile Phe Lys Gln Arg Arg Tyr Gly Leu Asp
 305 310 315 320
 Gly Gln Gln Ile Leu Val Tyr Lys Phe Arg Ser Met Thr Val Thr Glu
 325 330 335

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Asp Gly Ala Thr Val Thr Gln Ala Thr Arg Asn Asp Gln Arg Ile Thr
 340 345 350
 Pro Leu Gly Ala Phe Leu Arg Lys Thr Ser Leu Asp Glu Leu Pro Gln
 355 360 365
 Phe Ile Asn Val Leu Gln Gly Arg Met Ser Val Val Gly Pro Arg Pro
 370 375 380
 His Ala Val Ala His Asn Glu Glu Tyr Arg Lys Leu Ile Lys Gly Tyr
 385 390 395 400
 Met Val Arg His Lys Val Lys Pro Gly Ile Thr Gly Trp Ala Gln Val
 405 410 415
 Asn Gly Phe Arg Gly Glu Thr Asp Thr Leu Glu Lys Met Glu Gln Arg
 420 425 430
 Val His Tyr Asp Leu Glu Tyr Leu Arg Asn Trp Ser Pro Arg Leu Asp
 435 440 445
 Met Leu Ile Val Ala Lys Thr Ile Trp Leu Thr Ile Val Gly Gln Asp
 450 455 460
 Gly Ala Tyr
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<210> 3
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 <212> DNA
 <213> Methylophilus methylotrophus

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 acg cga tta tgg ccg ttg tca cgc gcg gtt ttg cct aaa cag tta ttg 96
 Thr Arg Leu Trp Pro Leu Ser Arg Ala Val Leu Pro Lys Gln Leu Leu
 20 25 30
 cct ttg gtg acc gaa aat acg atg tta cag gag aca ttg atc cgg ctt 144
 Pro Leu Val Thr Glu Asn Thr Met Leu Gln Glu Thr Leu Ile Arg Leu
 35 40 45
 tct agc tgg gcg gat gtc ggt cat cct atc gtc gtc tgt ggt aac gat 192
 Ser Ser Trp Ala Asp Val Gly His Pro Ile Val Val Cys Gly Asn Asp
 50 55 60
 cat cgc ttt ttg gtg gcg gag caa tta cgg caa gtg aat ttg aca cct 240
 His Arg Phe Leu Val Ala Glu Gln Leu Arg Gln Val Asn Leu Thr Pro
 65 70 75 80
 gag gcg att gtg ctg gag ccg gtg gcg cga aat acg gca cct gcg att 288
 Glu Ala Ile Val Leu Glu Pro Val Ala Arg Asn Thr Ala Pro Ala Ile
 85 90 95
 gct gct gcg gct gtg act tta aaa gac aaa gat gtc ttg atg ctg gtg 336
 Ala Ala Ala Ala Val Thr Leu Lys Asp Lys Asp Val Leu Met Leu Val
 100 105 110
 ttg cct gcg gat cat gtg att act gac gtc act gct ttt gag gct gct 384
 Leu Pro Ala Asp His Val Ile Thr Asp Val Thr Ala Phe Glu Ala Ala
 115 120 125
 gtg cgt cgt gcc tgc gtt gca gca gag cag ggg aaa ctg gtc aca ttt 432
 Val Arg Arg Ala Cys Val Ala Ala Glu Gln Gly Lys Leu Val Thr Phe

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130	135	140														
ggt	ata	gag	cct	aca	cag	ccg	gaa	acc	ggt	tat	ggt	tat	atc	caa	tca	480
Gly	Ile	Glu	Pro	Thr	Gln	Pro	Glu	Thr	Gly	Tyr	Gly	Tyr	Ile	Gln	Ser	
145					150				155							
ggt	gca	gaa	ttg	gaa	gca	tgt	gat	ggt	tgc	ttt	gaa	gtg	gca	cgt	ttt	528
Gly	Ala	Glu	Leu	Glu	Ala	Cys	Asp	Gly	Cys	Phe	Glu	Val	Ala	Arg	Phe	
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ggt	gag	aag	cct	gat	gct	gcg	act	gca	cag	caa	tat	ttg	gat	gcc	gga	576
Val	Glu	Lys	Pro	Asp	Ala	Ala	Thr	Ala	Gln	Gln	Tyr	Leu	Asp	Ala	Gly	
			180					185					190			
aac	ttt	tat	tgg	aac	agc	ggc	atg	ttt	ttg	ttt	aaa	ccg	gct	gtg	ttc	624
Asn	Phe	Tyr	Trp	Asn	Ser	Gly	Met	Phe	Leu	Phe	Lys	Pro	Ala	Val	Phe	
			195				200					205				
ctg	gct	gag	ttg	cag	caa	tac	gcg	cca	gcc	atg	gtc	agt	gcg	gta	agc	672
Leu	Ala	Glu	Leu	Gln	Gln	Tyr	Ala	Pro	Ala	Met	Val	Ser	Ala	Val	Ser	
			210			215						220				
aat	gcc	ggt	gcg	caa	agt	tat	aaa	gac	ctg	gat	ttt	gtg	cgc	ttg	cat	720
Asn	Ala	Val	Ala	Gln	Ser	Tyr	Lys	Asp	Leu	Asp	Phe	Val	Arg	Leu	His	
225					230				235					240		
gag	gcc	tcg	ttt	gct	gag	tct	cct	tct	gat	tca	att	gac	tat	gcc	gtc	768
Glu	Ala	Ser	Phe	Ala	Glu	Ser	Pro	Ser	Asp	Ser	Ile	Asp	Tyr	Ala	Val	
				245					250					255		
atg	gaa	aaa	acc	aaa	ctg	gcg	gcc	gtg	gta	cct	gcc	agc	atg	ggg	tggt	816
Met	Glu	Lys	Thr	Lys	Leu	Ala	Ala	Val	Val	Pro	Ala	Ser	Met	Gly	Trp	
			260					265					270			
aat	gat	ggt	ggc	tca	tggt	act	gcc	tta	aaa	gaa	gtg	cag	ccc	aat	gat	864
Asn	Asp	Val	Gly	Ser	Trp	Thr	Ala	Leu	Lys	Glu	Val	Gln	Pro	Asn	Asp	
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gcg	gat	ggg	aat	gct	aca	cggt	ggg	gat	gtg	ttt	ctt	aaa	aat	gtg	aaa	912
Ala	Asp	Gly	Asn	Ala	Thr	Arg	Gly	Asp	Val	Phe	Leu	Lys	Asn	Val	Lys	
290						295					300					
aat	acc	ttg	gta	cggt	gcgt	gaa	gag	cggt	ttt	gtg	gct	gcc	ggt	ggc	gta	960
Asn	Thr	Leu	Val	Arg	Ala	Glu	Glu	Arg	Phe	Val	Ala	Ala	Val	Gly	Val	
305					310				315						320	
gag	gat	ttg	ctg	att	ggt	gaa	acc	agt	gat	gcgt	atc	ctg	ggt	gcgt	cac	1008
Glu	Asp	Leu	Leu	Ile	Val	Glu	Thr	Ser	Asp	Ala	Ile	Leu	Val	Ala	His	
				325					330					335		
cgt	gat	tgt	gcgt	cag	gat	gtc	aag	aat	att	ggt	gat	cat	ttg	aag	gca	1056
Arg	Asp	Cys	Ala	Gln	Asp	Val	Lys	Asn	Ile	Val	Asp	His	Leu	Lys	Ala	
			340					345					350			
agc	gga	cgt	tct	gaa	cat	aag	atg	cat	ccc	cgt	ggt	tat	cgc	cct	tggt	1104
Ser	Gly	Arg	Ser	Glu	His	Lys	Met	His	Pro	Arg	Val	Tyr	Arg	Pro	Trp	
			355				360					365				
ggt	tggt	tac	gag	gga	atc	gat	atc	ggc	gag	cgt	ttc	cag	gtc	aag	cgt	1152
Gly	Trp	Tyr	Glu	Gly	Ile	Asp	Ile	Gly	Glu	Arg	Phe	Gln	Val	Lys	Arg	
						375					380					
att	atg	gtg	aaa	cca	gggt	gaa	aga	ttg	tca	ctg	caa	atg	cat	cat	cat	1200
Ile	Met	Val	Lys	Pro	Gly	Glu	Arg	Leu	Ser	Leu	Gln	Met	His	His	His	
385					390				395						400	
cgt	gct	gag	cac	tggt	gtt	gtc	agt	gggt	tct	gcc	atg	atc	act	att		1248
Arg	Ala	Glu	His	Trp	Val	Val	Val	Ser	Gly	Ala	Met	Ile	Thr	Ile		
				405					410				415			
gat	gat	gtc	acc	aag	ctc	tat	act	gaa	aac	gaa	tct	act	tat	ata	ccgt	1296
Asp	Asp	Val	Thr	Lys	Leu	Tyr	Thr	Glu	Asn	Glu	Ser	Thr	Tyr	Ile	Pro	
				420				425					430			

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att ggc tca acg cac cga cta gag aat cca ggt aaa ttg cct ttg cat	1344
Ile Gly Ser Thr His Arg Leu Glu Asn Pro Gly Lys Leu Pro Leu His	
435 440 445	
tta atc gag gtg caa tcc ggt agt tat ctt gga gaa gat gac atc gtg	1392
Leu Ile Glu Val Gln Ser Gly Ser Tyr Leu Gly Glu Asp Asp Ile Val	
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Arg Phe Glu Asp Thr Tyr Gly Arg Ser	
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<211> 473

<212> PRT

<213> Methylophilus methylotrophus

<400> 4

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Pro Leu Val Thr Glu Asn Thr Met Leu Gln Glu Thr Leu Ile Arg Leu	
35 40 45	
Ser Ser Trp Ala Asp Val Gly His Pro Ile Val Val Cys Gly Asn Asp	
50 55 60	
His Arg Phe Leu Val Ala Glu Gln Leu Arg Gln Val Asn Leu Thr Pro	
65 70 75 80	
Glu Ala Ile Val Leu Glu Pro Val Ala Arg Asn Thr Ala Pro Ala Ile	
85 90 95	
Ala Ala Ala Ala Val Thr Leu Lys Asp Lys Asp Val Leu Met Leu Val	
100 105 110	
Leu Pro Ala Asp His Val Ile Thr Asp Val Thr Ala Phe Glu Ala Ala	
115 120 125	
Val Arg Arg Ala Cys Val Ala Ala Glu Gln Gly Lys Leu Val Thr Phe	
130 135 140	
Gly Ile Glu Pro Thr Gln Pro Glu Thr Gly Tyr Gly Tyr Ile Gln Ser	
145 150 155 160	
Gly Ala Glu Leu Glu Ala Cys Asp Gly Cys Phe Glu Val Ala Arg Phe	
165 170 175	
Val Glu Lys Pro Asp Ala Ala Thr Ala Gln Gln Tyr Leu Asp Ala Gly	
180 185 190	
Asn Phe Tyr Trp Asn Ser Gly Met Phe Leu Phe Lys Pro Ala Val Phe	
195 200 205	
Leu Ala Glu Leu Gln Gln Tyr Ala Pro Ala Met Val Ser Ala Val Ser	
210 215 220	
Asn Ala Val Ala Gln Ser Tyr Lys Asp Leu Asp Phe Val Arg Leu His	
225 230 235 240	
Glu Ala Ser Phe Ala Glu Ser Pro Ser Asp Ser Ile Asp Tyr Ala Val	
245 250 255	
Met Glu Lys Thr Lys Leu Ala Ala Val Val Pro Ala Ser Met Gly Trp	
260 265 270	
Asn Asp Val Gly Ser Trp Thr Ala Leu Lys Glu Val Gln Pro Asn Asp	
275 280 285	
Ala Asp Gly Asn Ala Thr Arg Gly Asp Val Phe Leu Lys Asn Val Lys	
290 295 300	
Asn Thr Leu Val Arg Ala Glu Glu Arg Phe Val Ala Ala Val Gly Val	

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305	Glu	Asp	Leu	Leu	Ile	Val	Glu	Thr	Ser	Asp	Ala	Ile	Leu	Val	Ala	His
					325					330					335	
Arg	Asp	Cys	Ala	Gln	Asp	Val	Lys	Asn	Ile	Val	Asp	His	Leu	Lys	Ala	
			340					345					350			
Ser	Gly	Arg	Ser	Glu	His	Lys	Met	His	Pro	Arg	Val	Tyr	Arg	Pro	Trp	
		355					360					365				
Gly	Trp	Tyr	Glu	Gly	Ile	Asp	Ile	Gly	Glu	Arg	Phe	Gln	Val	Lys	Arg	
	370					375					380					
Ile	Met	Val	Lys	Pro	Gly	Glu	Arg	Leu	Ser	Leu	Gln	Met	His	His	His	
	385				390					395					400	
Arg	Ala	Glu	His	Trp	Val	Val	Val	Ser	Gly	Ser	Ala	Met	Ile	Thr	Ile	
				405					410					415		
Asp	Asp	Val	Thr	Lys	Leu	Tyr	Thr	Glu	Asn	Glu	Ser	Thr	Tyr	Ile	Pro	
			420					425					430			
Ile	Gly	Ser	Thr	His	Arg	Leu	Glu	Asn	Pro	Gly	Lys	Leu	Pro	Leu	His	
		435					440					445				
Leu	Ile	Glu	Val	Gln	Ser	Gly	Ser	Tyr	Leu	Gly	Glu	Asp	Asp	Ile	Val	
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer MgtfA-F1

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<210> 6
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 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: primer Km4-F2

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<210> 8
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 <212> DNA
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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer mManC-F1

 <400> 10
 ccgatccga tgcgtgtgcc tttagtc 27

 <210> 11
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer mManC-R1

 <400> 11
 ccgatccca cctaactacg gccgtagg 28

 <210> 12
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer mManC-F2

 <400> 12
 atttgaggtc ggtttgcttg cgctatttta acg 33

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<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer mManC-R2

<400> 13

tcgtgacata gcgttgacaca tagccctcat a

31